

What is claimed is:

1. A coryneform bacterium having L-glutamic acid producing ability, wherein trehalose synthesis ability is decreased or deleted in the bacterium.

5           2. The coryneform bacteria according to claim 1, wherein the trehalose synthesis ability is decreased or deleted by introducing a mutation into a chromosomal gene coding for an enzyme in trehalose synthesis pathway or disrupting the gene.

10           3. The coryneform bacteria according to claim 2, wherein the gene coding for the enzyme in trehalose synthesis pathway consists of a gene coding for trehalose-6-phosphate synthase, a gene coding for maltotriose synthase, or both of these genes.

15           4. The coryneform bacteria according to claim 3, wherein the gene coding for trehalose-6-phosphate synthase codes for the amino acid sequence of SEQ ID NO: 30, and the gene coding for maltotriose synthase codes for the amino acid sequence of SEQ ID NO:  
20           32.

          5. A method for producing L-glutamic acid comprising the steps of culturing a coryneform bacterium according to any one of claims 1-4 in a medium to produce and accumulate L-glutamic acid in the medium,  
25           and collecting the L-glutamic acid from the medium.

          6. A DNA coding for a protein defined in the following (A) or (B):

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(A) a protein having the amino acid sequence of  
SEQ ID NO: 30,

(B) a protein having the amino acid sequence of  
SEQ ID NO: 30 including substitution, deletion,  
5 insertion or addition of one or several amino acid  
residues and having trehalose-6-phosphate synthase  
activity.

7. A DNA according to claim 6, which is a DNA  
defined in the following (a) or (b):

10 (a) a DNA containing a nucleotide sequence  
comprising at least the residues of nucleotide numbers  
484-1938 in the nucleotide sequence of SEQ ID NO: 29,

(b) a DNA hybridizable with a nucleotide sequence  
comprising at least the residues of nucleotide numbers  
15 484-1938 in the nucleotide sequence of SEQ ID NO: 29  
under a stringent condition, showing homology of 55% or  
more to the foregoing nucleotide sequence, and coding  
for a protein having trehalose-6-phosphate synthase  
activity.

20 8. A DNA coding for a protein defined in the  
following (A) or (B):

(A) a protein having the amino acid sequence of  
SEQ ID NO: 32,

(B) a protein having the amino acid sequence of  
25 SEQ ID NO: 32 including substitution, deletion,  
insertion or addition of one or several amino acid  
residues and having maltooligosyltrehalose synthase

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activity.

9. A DNA according to claim 8, which is a DNA defined in the following (a) or (b):

(a) a DNA containing a nucleotide sequence  
5 comprising at least the residues of nucleotide numbers  
82-2514 in the nucleotide sequence of SEQ ID NO: 31,

(b) a DNA hybridizable with a nucleotide sequence  
comprising at least the residues of nucleotide numbers  
82-2514 in the nucleotide sequence of SEQ ID NO: 31  
10 under a stringent condition, showing homology of 60% or  
more to the foregoing nucleotide sequence, and coding  
for a protein having maltooligosyltrehalose synthase  
activity.

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